



AMD/C

SEQUENCE LISTING

<110> De Buyt, Eric
Lahaye, Andree
Ledoux, Pierre
Detroz, Rene

#3

<120> Xylanase, Microorganisms Producing it,
DNA Molecules, Methods for Preparing this Xylanase and Uses
of the Latter

<130> GC450-D1-US

<140> US 09/909,207

<141> 2001-07-19

<150> US 08/470,953

<151> 1995-06-06

<150> BE 09500448

<151> 1995-05-17

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<211> 663

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<213> Bacillus sp.

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caacaagttg	gtaacatgtc	cataaactac	ggagccaact	tccaaccaa	tggtaatgcg	240
tatttatgcg	tctatggttg	gactgttgac	cctcttgctg	aatattatat	tgctcgacagt	300
tggggcaact	ggcgtccacc	aggagcaacg	cctaagggga	ccatcactgt	tgatggagga	360
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tttaacaat	attggagtg	tcgaagatcg	aaacgcacga	gtggcacgat	ttctgtcagc	480
aaccacttta	gagcgtggga	aaacttaggg	atgaatatgg	ggaaaatgta	tgaagtcgcg	540
cttactgtag	aaggctatca	aagtagcgga	agtgctaattg	tatatagcaa	tacactaaga	600
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<210> 2

<211> 663

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)...(663)

<221> mat_peptide

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gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat	96
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His	
20 25 30	
ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc	144
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe	
35 40 45	
cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt	192
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly	
50 55 60	
aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg	240
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala	
65 70 75 80	
tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat	288
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr	
85 90 95	
att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag	336
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys	
100 105 110	
ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt	384
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu	
115 120 125	
aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat	432
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr	
130 135 140	
tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc	480
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser	
145 150 155 160	
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Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met	
165 170 175	
tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct	576
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala	
180 185 190	
aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act	624
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr	
195 200 205	
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210 215 220	

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<211> 221
 <212> PRT
 <213> Bacillus sp.

<400> 3

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Gly	Gly	Thr	Phe	Ser	Ala	Gln	Trp	Asn	Asn	Val	Asn	Asn	Ile	Leu	Phe
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	65				70				75						80
Tyr	Leu	Cys	Val	Tyr	Gly	Trp	Thr	Val	Asp	Pro	Leu	Val	Glu	Tyr	Tyr
			85					90					95		
Ile	Val	Asp	Ser	Trp	Gly	Asn	Trp	Arg	Pro	Pro	Gly	Ala	Thr	Pro	Lys
		100						105					110		
Gly	Thr	Ile	Thr	Val	Asp	Gly	Gly	Thr	Tyr	Asp	Ile	Tyr	Glu	Thr	Leu
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Arg	Val	Asn	Gln	Pro	Ser	Ile	Lys	Gly	Ile	Ala	Thr	Phe	Lys	Gln	Tyr
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Trp	Ser	Val	Arg	Arg	Ser	Lys	Arg	Thr	Ser	Gly	Thr	Ile	Ser	Val	Ser
	145				150				155						160
Asn	His	Phe	Arg	Ala	Trp	Glu	Asn	Leu	Gly	Met	Asn	Met	Gly	Lys	Met
			165					170					175		
Tyr	Glu	Val	Ala	Leu	Thr	Val	Glu	Gly	Tyr	Gln	Ser	Ser	Gly	Ser	Ala
			180					185					190		
Asn	Val	Tyr	Ser	Asn	Thr	Leu	Arg	Ile	Asn	Gly	Asn	Pro	Leu	Ser	Thr
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<210> 4
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 <212> DNA
 <213> Bacillus sp.

<400> 4

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tatgattatg	aatttttgaa	agatagcggg	ggctctggga	caatgattct	caatcatggc	180
ggtacgttca	gtgcccaatg	gaacaatgtt	aacaacatat	tattccgtaa	aggtaaaaaa	240
ttcaatgaaa	cacaaacaca	ccaacaagtt	ggtaacatgt	ccataaacta	cggagccaac	300
ttccaaccaa	atggtaatgc	gtattttatgc	gtctatgggt	ggactgttga	ccctcttgtc	360
gaatattata	ttgtcgacag	ttggggcaac	tggcgteccac	caggagcaac	gcctaagggg	420
accatcactg	ttgatggagg	aacatatgat	atctacgaga	ctcttagagt	caatcaaccc	480
tccattaagg	ggattgccac	atttaaacaa	tattggagtg	ttcgaagatc	gaaacgcacg	540
agtggcacga	tttctgtcag	caaccacttt	agagcgtggg	aaaacttagg	gatgaatatg	600
gggaaaatgt	atgaagtcgc	gcttactgta	gaaggctatc	aaagtagcgg	aagtgctaata	660
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 <212> DNA
 <213> Bacillus sp.

<220>

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 <222> (1)...(744)

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 gca cta acc tta cct gca gaa ata att cag gca caa atc gtc acc gac 96
 Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
 20 25 30
 aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat 144
 Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
 35 40 45
 agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt 192
 Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
 50 55 60
 gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa 240
 Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
 65 70 75 80
 ttc aat gaa aca caa aca cac caa caa gtt ggt aac atg tcc ata aac 288
 Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
 85 90 95
 tac gga gcc aac ttc caa cca aat ggt aat gcg tat tta tgc gtc tat 336
 Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
 100 105 110
 ggt tgg act gtt gac cct ctt gtc gaa tat tat att gtc gac agt tgg 384
 Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
 115 120 125
 ggc aac tgg cgt cca cca gga gca acg cct aag ggg acc atc act gtt 432
 Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
 130 135 140
 gat gga gga aca tat gat atc tac gag act ctt aga gtc aat caa ccc 480
 Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
 145 150 155 160
 tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga 528
 Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
 165 170 175
 tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg 576
 Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
 180 185 190
 tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt 624
 Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu

195	200	205	
act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat			672
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn			
210	215	220	
aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag			720
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu			
225	230	235	240
agc ata act ttg gat aaa aac aat			744
Ser Ile Thr Leu Asp Lys Asn Asn			
245			

<210> 6
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 <212> PRT
 <213> Bacillus sp.

<400> 6

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20	25	30	
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp			
35	40	45	
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser			
50	55	60	
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys			
65	70	75	80
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn			
85	90	95	
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr			
100	105	110	
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp			
115	120	125	
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val			
130	135	140	
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro			
145	150	155	160
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg			
165	170	175	
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala			
180	185	190	
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu			
195	200	205	
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn			
210	215	220	
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu			
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Ser Ile Thr Leu Asp Lys Asn Asn			
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 <212> DNA
 <213> Bacillus sp.

<400> 7

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<211> 81
<212> DNA
<213> Bacillus sp.

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<222> (1)...(81)

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gca cta acc tta cct gca gaa ata att cag gca 81
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<210> 9
<211> 27
<212> PRT
<213> Bacillus sp.

<400> 9
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<211> 1513
<212> DNA
<213> Bacillus sp.

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ataggaactt tcccatttgc aagacgataa aaaatcctttt tcccctattt tatcttatcg 180
ccttgatcgg tttaatttgt aaactttatt ttagttttacg tgatgttccc tcattcatac 240
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agcagctatc caaaaaacac tgatgttgac ctcttaaaga agtgtcacta tctatgaaaa 480
gataattatc cagtttcaaa atttgaaata gtgtgtatgg aatagtttga atgtcaactg 540
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aagtagcgga	agtgctaattg	tatatagcaa	tacactaaga	attaacggta	accctctctc	1320
aactattagt	aatgacgaga	gcataacttt	ggataaaaac	aattaaaaat	ccttatctct	1380
ttcggttcag	ttctcattat	tttcaaataa	cctccccggt	ggatcttttc	caacgggagg	1440
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<211> 1513

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (620)...(1363)

<221> mat_peptide

<222> (701)...(1363)

<221> sig_peptide

<222> (620)...(700)

<400> 11

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cattaatcac	agttaacgct	agagtcacat	tttttcgggt	ctcaaaaata	cctgaagaac	300
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ttaaaaggag	gaatgccta	atg aga caa	aag aaa ttg	acg ttg att	tta gcc	652
	Met Arg Gln	Lys Lys Leu	Thr Leu Ile	Leu Ala		
	1	5	10			

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Phe Leu Val Cys Phe Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala	
15 20 25	

caa atc gtc acc gac aat tcc att ggc aac cac gat ggc tat gat tat	748
Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr	
30 35 40	

gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat	796
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His	
45 50 55	

ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc	844
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe	
60 65 70 75	

cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt	892
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly	
80 85 90	

aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg	940
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Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala	
95 100 105	
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Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr	
110 115 120	
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Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys	
125 130 135	
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Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu	
140 145 150 155	
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Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr	
160 165 170	
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175 180 185	
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Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met	
190 195 200	
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Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala	
205 210 215	
aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act	1324
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr	
220 225 230 235	
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Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn	
240 245	
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 <212> DNA
 <213> Bacillus sp.

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ataggaactt tcccatttgc aagacgataa aaaatctttt tcccctatatt tatcttatcg	180
ccttgatcgg tttaatttgt aaactttatt ttagtttacg tgatgttccc tcattcatac	240
cattaatcac agttaacgct agagtcactt tttttcggtt ctcaaaaata cctgaagaac	300
atttatgtca tattttctca cgccgctcca taatggaata tatatactct tttatacata	360
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gataattatc cagttttcaaa atttgaaata gtgtgtatgg aatagtttga atgtcaactg	540
ctgtgaaagg agggtaggta gtaccgtaga cttcattacc aaaaattagt tgtaaaaaaa	600
ttaaaaggag gaatgccta	619

<210> 13
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 <212> DNA
 <213> Bacillus sp.

<400> 13
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 gaggaatgct tgaaacacct ccgtcactag 150

<210> 14
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 14
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<210> 15
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

<400> 15
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			20					25							